

**gsem model description options** — Model description options

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## Description

*paths* and the options above describe the model to be fit by `gsem`.

## Syntax

`gsem` *paths* ..., ... *model\_description\_options*

<i>model_description_options</i>	Description
<code>family()</code> , <code>link()</code> , ...	see <a href="#">[SEM] gsem family-and-link options</a>
* <code>covariance()</code>	path notation for treatment of covariances; see <a href="#">[SEM] sem and gsem path notation</a>
* <code>variance()</code>	path notation for treatment of variances; see <a href="#">[SEM] sem and gsem path notation</a>
* <code>means()</code>	path notation for treatment of means; see <a href="#">[SEM] sem and gsem path notation</a>
* <code>covstructure()</code>	alternative method to place restrictions on covariances; see <a href="#">[SEM] sem and gsem option covstructure()</a>
<code>collinear</code>	keep collinear variables
<code>noconstant</code>	do not fit intercepts
<code>noasis</code>	omit perfect predictors from Bernoulli models
<code>noanchor</code>	do not apply default anchoring
<code>forcenoanchor</code>	programmer's option
* <code>reliability()</code>	reliability of measurement variables; see <a href="#">[SEM] sem and gsem option reliability()</a>
<code>constraints()</code>	specify constraints; see <a href="#">[SEM] sem and gsem option constraints()</a>
<code>from()</code>	specify starting values; see <a href="#">[SEM] sem and gsem option from()</a>

\* Option may be specified more than once.

## Options

`family()` and `link()` specify the distribution and link function, such as `family(poisson)` `link(log)`, for generalized linear responses. There are lots of synonyms, so you can specify, for example, just `poisson`. In addition, there are `exposure()` and `offset()` options. See [\[SEM\] gsem family-and-link options](#).

`covariance()`, `variance()`, and `means()` fully describe the model to be fit. See [\[SEM\] sem and gsem path notation](#).

`covstructure()` provides a convenient way to constrain covariances in your model. Alternatively or in combination, you can place constraints by using the standard path notation. See [SEM] [sem and gsem option covstructure\(\)](#).

`collinear`; see [R] [estimation options](#).

`noconstant` specifies that all intercepts be constrained to 0. See [SEM] [sem and gsem path notation](#).

This option is seldom specified.

`noasis` specifies that perfect-predictor variables be omitted from all family Bernoulli models. By default, `gsem` does not omit the variable, so one can specify tricky models where an equation contains perfect predictors that are still identified through other portions of the model.

`noanchor` specifies that `gsem` not check for lack of identification or fill in anchors where needed. `gsem` is instead to issue an error message if anchors would be needed. Specify this option when you believe you have specified the necessary normalization constraints and want to hear about it if you are wrong. See *Identification 2: Normalization constraints (anchoring)* in [SEM] [intro 4](#).

`forcenoanchor` is similar to `noanchor` except that rather than issue an error message, `gsem` proceeds to estimation. There is no reason you should specify this option. `forcenoanchor` is used in testing of `gsem` at StataCorp.

`reliability()` specifies the fraction of variance not due to measurement error for a variable. See [SEM] [sem and gsem option reliability\(\)](#).

`constraints()` specifies parameter constraints you wish to impose on your model; see [SEM] [sem and gsem option constraints\(\)](#). Constraints can also be specified as described in [SEM] [sem and gsem path notation](#), and they are usually more conveniently specified using the path notation.

`from()` specifies the starting values to be used in the optimization process; see [SEM] [sem and gsem option from\(\)](#). Starting values can also be specified using the `init()` suboption as described in [SEM] [sem and gsem path notation](#).

## Remarks and examples

[stata.com](http://www.stata.com)

To use `gsem` successfully, you need to understand *paths*, `covariance()`, `variance()`, and `means()`; see *Using path diagrams to specify standard linear SEMs* in [SEM] [intro 2](#) and see [SEM] [sem and gsem path notation](#).

`covstructure()` is often convenient; see [SEM] [sem and gsem option covstructure\(\)](#).

## Also see

[SEM] [gsem](#) — Generalized structural equation model estimation command

[SEM] [intro 2](#) — Learning the language: Path diagrams and command language

[SEM] [sem and gsem option constraints\(\)](#) — Specifying constraints

[SEM] [sem and gsem option covstructure\(\)](#) — Specifying covariance restrictions

[SEM] [sem and gsem option from\(\)](#) — Specifying starting values

[SEM] [sem and gsem option reliability\(\)](#) — Fraction of variance not due to measurement error

[SEM] [sem and gsem path notation](#) — Command syntax for path diagrams